

570
12/1

#8

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/932,227

DATE: 12/03/2001
 TIME: 10:52:53

Input Set : A:\58715-A-PCT-US.txt
 Output Set: N:\CRF3\11212001\I932227.raw

P.5
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3 <110> APPLICANT: VOSSHALL, LESLIE
4     AMREIN, HUBERT
5     AXEL, RICHARD
7 <120> TITLE OF INVENTION: GENES ENCODING INSECT ODORANT RECEPTORS AND USES THEREOF
9 <130> FILE REFERENCE: 0575/58715-A-PCT-US/JPW/ADM/BJA
11 <140> CURRENT APPLICATION NUMBER: US 09/932,227
12 <141> CURRENT FILING DATE: 2001-08-17
14 <150> PRIOR APPLICATION NUMBER: PCT/US00/04995
15 <151> PRIOR FILING DATE: 2000-02-25
17 <160> NUMBER OF SEQ ID NOS: 108
19 <170> SOFTWARE: PatentIn version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1285
23 <212> TYPE: DNA
24 <213> ORGANISM: DROSOPHILA MELANOGASTER DOR62
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29 gtttgggagc tcaactggcct gatgcgtcct cggggcggtt caagcctgct ttacgtggta      120
31 tactccaatta cgggtcaactt ggtgggtcacc gtgctgtttc ccttgagctt gctggccagg      180
33 ctgctgttca ccaccaacat ggccggattg tgcgagaacc tgaccataac tattaccgat      240
35 attgtggcca atttgaagtt tgcgaatgtg tacatggtga ggaagcagct ccatgagatt      300
37 cgctctctcc taaggtcat ggacgctaga gcccggttg tggcgatcc cgaggagatt      360
39 tctgccttga ggaaggaagt gaatatcgca cagggcactt tccgcacct tgccagtatt      420
41 ttcgtatttg gcactacttt gagttgcgtc cgcgtggtcg ttcgccgga tcgagagctc      480
43 ctgtatccgg cctggttcgg cgttgactgg atgcactcca ccagaaacta tgtgtcatc      540
45 aatatctacc agctcttcgg cttgatagtg caggctatac agaactgcgc tagtgactcc      600
47 tatccgcctg cgtttctctg cctgctcacg ggtcatatgc gtgctttgga gctgagggtg      660
49 cggcggattg gctgcaggac ggaaaagtcc aataaagggc agacatatga agcctggcgg      720
51 gaggaggtgt accaggaact catcgagtgc atccgcgac tggcgcgggt ccatcggtg      780
53 agggagatca ttcagcgggt cctttcagtg ccctgcatgg cccagttcgt ctgctccgcc      840
55 gccgtccagt gtaccgtcgc catgcacttc ctgtacgtag cggatgacca cgaccacacc      900
57 gccatgatca tctcgattgt atttttctcg gccgtcacct tggaggtgtt tgtaatctgc      960
59 tattttgggg acaggatgcg gacacagagc gaggcgctgt gcgatgcctt ctacgattgc      1020
61 aactggatag aacagctgcc caagttcaag cgcgaactgc tcttcaccct ggccaggacg      1080
63 cagcggcctt ctcttattta cgcaggcaac tacatcgcac tctcgtgga gaccttcgag      1140
65 caggtcatga ggttcacata ctctgttttc aactcttgcc tgagggccaa gtaagaactt      1200
67 tataatctct ttttggggag aaaaatttta aagcacaata gcagaaaaat atatcagata      1260
69 atataacaaa aaaaaaaaaa aaaaaa      1285
72 <210> SEQ ID NO: 2
73 <211> LENGTH: 397
74 <212> TYPE: PRT
75 <213> ORGANISM: DROSOPHILA MELANOGASTER DOR62
77 <400> SEQUENCE: 2
79 Met Glu Lys Gln Glu Asp Phe Lys Leu Asn Thr His Ser Ala Val Tyr
80 1           5           10           15
82 Tyr His Trp Arg Val Trp Glu Leu Thr Gly Leu Met Arg Pro Pro Gly
83           20           25           30

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85 Val Ser Ser Leu Leu Tyr Val Val Tyr Ser Ile Thr Val Asn Leu Val
86      35      40      45
88 Val Thr Val Leu Phe Pro Leu Ser Leu Leu Ala Arg Leu Leu Phe Thr
89      50      55      60
91 Thr Asn Met Ala Gly Leu Cys Glu Asn Leu Thr Ile Thr Ile Thr Asp
92 65      70      75      80
94 Ile Val Ala Asn Leu Lys Phe Ala Asn Val Tyr Met Val Arg Lys Gln
95      85      90      95
97 Leu His Glu Ile Arg Ser Leu Leu Arg Leu Met Asp Ala Arg Ala Arg
98      100     105     110
100 Leu Val Gly Asp Pro Glu Glu Ile Ser Ala Leu Arg Lys Glu Val Asn
101      115     120     125
103 Ile Ala Gln Gly Thr Phe Arg Thr Phe Ala Ser Ile Phe Val Phe Gly
104      130     135     140
106 Thr Thr Leu Ser Cys Val Arg Val Val Val Arg Pro Asp Arg Glu Leu
107 145     150     155     160
109 Leu Tyr Pro Ala Trp Phe Gly Val Asp Trp Met His Ser Thr Arg Asn
110      165     170     175
112 Tyr Val Leu Ile Asn Ile Tyr Gln Leu Phe Gly Leu Ile Val Gln Ala
113      180     185     190
115 Ile Gln Asn Cys Ala Ser Asp Ser Tyr Pro Pro Ala Phe Leu Cys Leu
116      195     200     205
118 Leu Thr Gly His Met Arg Ala Leu Glu Leu Arg Val Arg Arg Ile Gly
119      210     215     220
121 Cys Arg Thr Glu Lys Ser Asn Lys Gly Gln Thr Tyr Glu Ala Trp Arg
122 225     230     235     240
124 Glu Glu Val Tyr Gln Glu Leu Ile Glu Cys Ile Arg Asp Leu Ala Arg
125      245     250     255
127 Val His Arg Leu Arg Glu Ile Ile Gln Arg Val Leu Ser Val Pro Cys
128      260     265     270
130 Met Ala Gln Phe Val Cys Ser Ala Ala Val Gln Cys Thr Val Ala Met
131      275     280     285
133 His Phe Leu Tyr Val Ala Asp Asp His Asp His Thr Ala Met Ile Ile
134      290     295     300
136 Ser Ile Val Phe Phe Ser Ala Val Thr Leu Glu Val Phe Val Ile Cys
137 305     310     315     320
139 Tyr Phe Gly Asp Arg Met Arg Thr Gln Ser Glu Ala Leu Cys Asp Ala
140      325     330     335
142 Phe Tyr Asp Cys Asn Trp Ile Glu Gln Leu Pro Lys Phe Lys Arg Glu
143      340     345     350
145 Leu Leu Phe Thr Leu Ala Arg Thr Gln Arg Pro Ser Leu Ile Tyr Ala
146      355     360     365
148 Gly Asn Tyr Ile Ala Leu Ser Leu Glu Thr Phe Glu Gln Val Met Arg
149      370     375     380
151 Phe Thr Tyr Ser Val Phe Thr Leu Leu Leu Arg Ala Lys
152 385     390     395
154 <210> SEQ ID NO: 3
155 <211> LENGTH: 1499
156 <212> TYPE: DNA

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Input Set : A:\58715-A-PCT-US.txt

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157 <213> ORGANISM: DROSOPHILA MELANOGASTER DOR104

159 <400> SEQUENCE: 3

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160 gaattcggca cgagcagtcg atggccagtc ttcagttcca cggcaacgtc gatgcggaca      60
162 tcaggtatga tattagcctg gatccggcta gggaaatcgaa tctcttccgt ctgctaattgg      120
164 gactccagtt ggcgaatggc acgaagccat cgccgcggtt acccaaattg tggccaaagc      180
166 ggctggaaat gattggtaaa gtgctgcccc aagcctattg ttccatggtg atttttcacct      240
168 ccctgcattt ggggtgcctg ttcacgaaaa ccacactgga tgtcctgccg acggggggagc      300
170 tgcaggccat aacggatgcc ctcaccatga ccataatata ctttttcacg ggctacggca      360
172 ccatctactg gtgcctgcgc tcccggcgcc tcttggccta catggagcac atgaaccggg      420
174 agtatcgcca tcattcgctg gccgggggtga cctttgtgag tagccatgog gccttttagga      480
176 tgtccagaaa cttcacggtg gtgtggataa tgtcctgcct gctgggogtg atttcctggg      540
178 gcgtttcgcc actgatgctg ggcatccgga tgctgccgct ccaatgttggt tatcccttcg      600
180 acgccctggg tcccggcaca tatacggcgg tctatgctac acaacttttc ggtcagatca      660
182 tgggtgggcat gacctttgga ttcgggggat cactgtttgt caccctgagc ctgctactcc      720
184 tgggacaatt cgatgtgctc tactgcagcc tgaagaacct ggatgccccat accaagttgc      780
186 tgggcgggga gtctgtaaat ggctgagtt cgctgcaaga ggagttgctg ctggggggact      840
188 cgaagaggga attaaatcag tacgttttgc tccaggagca tccgacggat ctgctgagat      900
190 tgtcggcagg acgaaaatgt cctgaccaag gaaatgcgtt tcacaacgcc ttggtggaat      960
192 gcattcgctt gcctcgcttc attctgcact gctcacagga gttggagaat ctattcagtc     1020
194 catattgtct ggtcaagtca ctgcagatca cctttcagct ttgcctgctg gtctttgtgg     1080
196 gcgtttcggg tactcgagag gtctgcgga ttgtcaacca gctacagtac ttgggactga     1140
198 ccatcttcga gctcctaatt ttcacctatt gtggcgaaact cctcagtcgg catagtattc     1200
200 gatctggcga cgccttttgg aggggtgcgt ggtggaagca cgcctatttc atccgccagg     1260
202 acatcctcat ctttctgtgc aatagtagac gtgcagttca cgtgactgcc ggcaagtttt     1320
204 atgtgatgga tgtgaatcgt ctaagatcgg ttataacgca ggcgttcagc ttcttgactt     1380
206 tgctgcaaaa gttggctgcc aagaagacgg aatcggagct ctaaaactggt accacgcacg     1440
208 gatatttatt tagcgcatta aaaaaaagtc gagtaaaagc aaaaaaaaaa aaaaaaaaaa     1499

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211 <210> SEQ ID NO: 4

212 <211> LENGTH: 467

213 <212> TYPE: PRT

214 <213> ORGANISM: DROSOPHILA MELANOGASTER DOR104

216 <400> SEQUENCE: 4

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218 Met Ala Ser Leu Gln Phe His Gly Asn Val Asp Ala Asp Ile Arg Tyr
219 1      5      10      15
221 Asp Ile Ser Leu Asp Pro Ala Arg Glu Ser Asn Leu Phe Arg Leu Leu
222      20      25      30
224 Met Gly Leu Gln Leu Ala Asn Gly Thr Lys Pro Ser Pro Arg Leu Pro
225      35      40      45
227 Lys Trp Trp Pro Lys Arg Leu Glu Met Ile Gly Lys Val Leu Pro Lys
228      50      55      60
230 Ala Tyr Cys Ser Met Val Ile Phe Thr Ser Leu His Leu Gly Val Leu
231 65      70      75      80
233 Phe Thr Lys Thr Thr Leu Asp Val Leu Pro Thr Gly Glu Leu Gln Ala
234      85      90      95
236 Ile Thr Asp Ala Leu Thr Met Thr Ile Ile Tyr Phe Phe Thr Gly Tyr
237      100     105     110
239 Gly Thr Ile Tyr Trp Cys Leu Arg Ser Arg Arg Leu Leu Ala Tyr Met
240      115     120     125
242 Glu His Met Asn Arg Glu Tyr Arg His His Ser Leu Ala Gly Val Thr

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243      130      135      140
245 Phe Val Ser Ser His Ala Ala Phe Arg Met Ser Arg Asn Phe Thr Val
246 145      150      155      160
248 Val Trp Ile Met Ser Cys Leu Leu Gly Val Ile Ser Trp Gly Val Ser
249      165      170      175
251 Pro Leu Met Leu Gly Ile Arg Met Leu Pro Leu Gln Cys Trp Tyr Pro
252      180      185      190
254 Phe Asp Ala Leu Gly Pro Gly Thr Tyr Thr Ala Val Tyr Ala Thr Gln
255      195      200      205
257 Leu Phe Gly Gln Ile Met Val Gly Met Thr Phe Gly Phe Gly Gly Ser
258      210      215      220
260 Leu Phe Val Thr Leu Ser Leu Leu Leu Leu Gly Gln Phe Asp Val Leu
261 225      230      235      240
263 Tyr Cys Ser Leu Lys Asn Leu Asp Ala His Thr Lys Leu Leu Gly Gly
264      245      250      255
266 Glu Ser Val Asn Gly Leu Ser Ser Leu Gln Glu Glu Leu Leu Gly
267      260      265      270
269 Asp Ser Lys Arg Glu Leu Asn Gln Tyr Val Leu Leu Gln Glu His Pro
270      275      280      285
272 Thr Asp Leu Leu Arg Leu Ser Ala Gly Arg Lys Cys Pro Asp Gln Gly
273      290      295      300
275 Asn Ala Phe His Asn Ala Leu Val Glu Cys Ile Arg Leu His Arg Phe
276 305      310      315      320
278 Ile Leu His Cys Ser Gln Glu Leu Glu Asn Leu Phe Ser Pro Tyr Cys
279      325      330      335
281 Leu Val Lys Ser Leu Gln Ile Thr Phe Gln Leu Cys Leu Leu Val Phe
282      340      345      350
284 Val Gly Val Ser Gly Thr Arg Glu Val Leu Arg Ile Val Asn Gln Leu
285      355      360      365
287 Gln Tyr Leu Gly Leu Thr Ile Phe Glu Leu Leu Met Phe Thr Tyr Cys
288      370      375      380
290 Gly Glu Leu Leu Ser Arg His Ser Ile Arg Ser Gly Asp Ala Phe Trp
291 385      390      395      400
293 Arg Gly Ala Trp Trp Lys His Ala His Phe Ile Arg Gln Asp Ile Leu
294      405      410      415
296 Ile Phe Leu Val Asn Ser Arg Arg Ala Val His Val Thr Ala Gly Lys
297      420      425      430
299 Phe Tyr Val Met Asp Val Asn Arg Leu Arg Ser Val Ile Thr Gln Ala
300      435      440      445
302 Phe Ser Phe Leu Thr Leu Leu Gln Lys Leu Ala Ala Lys Lys Thr Glu
303      450      455      460
305 Ser Glu Leu
306 465
308 <210> SEQ ID NO: 5
309 <211> LENGTH: 1556
310 <212> TYPE: DNA
311 <213> ORGANISM: DROSOPHILA MELANOGASTER DOR87
313 <400> SEQUENCE: 5
314 ggcacgaggc ttatagaaag tgccgagcaa tgacaatcga ggatatcggc ctggtgggca

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60

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316 tcaacgtgcg gatgtggcga cacttgccgc tgctgtaccc cactccgggc tccagctggc 120
318 gcaagttcgc cttcgtgctg ccggtgactg cgatgaatct gatgcagttc gtctacctgc 180
320 tgcggatgtg gggcgacctg cccgccttca ttctgaacat gttcttcttc tcggccattt 240
322 tcaacgccct gatgcgacg tggtgggtca taatcaagcg gcgccagttc gaggagtctc 300
324 tcggccaact ggccactctg ttccattcga ttctcgactc caccgacgag tggggcgctg 360
326 gcacccctgcg gagggcgga cgggaggctc ggaacctggc catccttaat ttgagtgcct 420
328 ccttcctgga cattgtcggg gctctgggat cgccgctttt cagggaggag agagctatc 480
330 ccttcggcgt agctctacca ggagtgcga tgaccagttc acccgtctac gaggttatct 540
332 acttgcccca actgcctacg cccctgctgc tgtccatgat gtacatgcct ttcgtcagcc 600
334 tttttgcgg cctggccatc tttgggaagg ccatgctgca gatcctggta cacaggctgg 660
336 gccagattgg cggagaagag cagtcggagg aggagcgctt ccaaaggctg gcctcctgca 720
338 ttgcgtacca cacgcaggtg atgcgctatg tgtggcagct caacaaactg gtggccaaca 780
340 ttgtggcggg ggaagcaatt atttttggct cgataatctg ctactgctc ttctgtctga 840
342 atattataac ctcaccacc caggtgatct cgatagtgat gtacattctg accatgctgt 900
344 acgttctctt cacctactac aatcgggcca atgaaatatg cctcgagaac aaccgggtgg 960
346 cggaggctgt ttacaatgtg ccctggtacg aggcaggaac tcggtttcgc aaaacctcc 1020
348 tgatcttctt gatgcaaaaca caacaccga tggagataag agtcggcaac gtttacccca 1080
350 tgacattggc catgttccag agtctgttga atgcgtccta ctctacttt accatgctgc 1140
352 gtggcgctac cggcaaatga gctgaaagac cgaaaaaacc ggagtatccc ctccatatt 1200
354 cccctgctc ctttattttt ctttccctt cctttccgt tttccattc gctttccag 1260
356 caatccgggt aatgcaaaaa gttgttgcgt gctgtggtcc tggctgctt tttggcattt 1320
358 gcatatgctt gtcgtttgaa aggatttaat cggactgctg gcacggagtc ggcacctgg 1380
360 ctccctggatc ctggcatgca aatagtggc ttcttagatt gttacacaaa atagattgta 1440
362 gattgcagct gaatgttgtg cttggaataa agtcaaaagg atgtggagtc ggccaaggc 1500
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368 <211> LENGTH: 376

369 <212> TYPE: PRT


370 <213> ORGANISM: DROSOPHILA MELANOGASTER DOR87

372 <400> SEQUENCE: 6

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375 1 5 10 15
377 Arg His Leu Ala Val Leu Tyr Pro Thr Pro Gly Ser Ser Trp Arg Lys
378 20 25 30
380 Phe Ala Phe Val Leu Pro Val Thr Ala Met Asn Leu Met Gln Phe Val
381 35 40 45
383 Tyr Leu Leu Arg Met Trp Gly Asp Leu Pro Ala Phe Ile Leu Asn Met
384 50 55 60
386 Phe Phe Phe Ser Ala Ile Phe Asn Ala Leu Met Arg Thr Trp Leu Val
387 65 70 75 80
389 Ile Ile Lys Arg Arg Gln Phe Glu Glu Phe Leu Gly Gln Leu Ala Thr
390 85 90 95
392 Leu Phe His Ser Ile Leu Asp Ser Thr Asp Glu Trp Gly Arg Gly Ile
393 100 105 110
395 Leu Arg Arg Ala Glu Arg Glu Ala Arg Asn Leu Ala Ile Leu Asn Leu
396 115 120 125
398 Ser Ala Ser Phe Leu Asp Ile Val Gly Ala Leu Val Ser Pro Leu Phe
399 130 135 140
401 Arg Glu Glu Arg Ala His Pro Phe Gly Val Ala Leu Pro Gly Val Ser

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 Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\58715-A-PCT-US.txt

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L:6893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:108